

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Wackett, Lawrence P.
Sadowsky, Michael J.
de Souza, Mervyn L.

(ii) TITLE OF INVENTION: An Isolated and Purified DNA Molecule
and Protein for the Degradation of Triazine Compounds

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
(B) STREET: P.O. Box 581415
(C) CITY: Minneapolis
(D) STATE: MN
(E) COUNTRY: USA
(F) ZIP: 55458-1415

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mueting, Ann M.
(B) REGISTRATION NUMBER: 33,977
(C) REFERENCE/DOCKET NUMBER: 110.00230101

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 612-305-1217
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGGGTAAC	TTCTTGAGCG	CGGCCACAGC	AGCCTTGATC	ATGAAGGCGA	GCATGGTGAC	60
CTTGACGCCG	CTCTTTCGT	TCTCTTGTT	GAACTCACG	CGAAAGGCTT	CCAGGTCGGT	120
GATGTCCGCG	TCGTCGTGGT	TGGTGACGTG	CGGGATGACC	ACCCAGTTGC	GGTGCAGGTT	180
TTTCGATGGC	ATAATATCTG	CGTTGCGACG	TGTAACACAC	TATTGGAGAC	ATATCATGCA	240
AACGCTCAGC	ATCCAGCACG	GTACCCTCGT	CACGATGGAT	CAGTACCGCA	GAGTCCTTGG	300
GGATAGCTGG	GTTCACGTGC	AGGATGGACG	GATCGTCGCG	CTCGGAGTGC	ACGCCGAGTC	360
GGTGCCTCCG	CCAGCGGATC	GGGTGATCGA	TGCACGCGGC	AAGGTCGTGT	TACCCGGTTT	420
CATCAATGCC	CACACCCATG	TGAACCAGAT	CCTCCTGCGC	GGAGGGCCCT	CGCACGGACG	480
TCAATTCTAT	GACTGGCTGT	TCAACGTTGT	GTATCCGGGA	CAAAAGGCGA	TGAGACCGGA	540
GGACGTAGCG	GTGGCGGTGA	GGTTGTATTG	TGCGGAAGCT	GTGCGCAGCG	GGATTACGAC	600
GATCAACGAA	AACGCCGATT	CGGCCATCTA	CCCAGGCAAC	ATCGAGGCCG	CGATGGCGGT	660
CTATGGTGAG	GTGGGTGTGA	GGGTCGTCTA	CGCCCGCATG	TTCTTGATC	GGATGGACGG	720
GCGCATTCAA	GGGTATGTGG	ACGCCTTGAA	GGCTCGCTCT	CCCCAAGTCG	AACTGTGCTC	780
GATCATGGAG	GAAACGGCTG	TGGCCAAAGA	TCGGATCACA	GCCCTGTCAG	ATCAGTATCA	840
TGGCACGGCA	GGAGGTCGTA	TATCAGTTG	GCCCCGTCCT	GCCACTACCA	CGGGCGGTGAC	900
AGTTGAAGGA	ATGCGATGGG	CACAAGCCTT	CGCCCGTGAT	CGGGCGGTAA	TGTGGACGCT	960
TCACATGGCG	GAGAGCGATC	ATGATGAGCG	GATTCAATGGG	ATGAGTCCCG	CCGAGTACAT	1020
GGAGTGTTAC	GGACTCTTGG	ATGAGCGTCT	GCAGGTCGCG	CATTGCGTGT	ACTTGACCG	1080
GAAGGATGTT	CGGCTGCTGC	ACCGCCACAA	TGTGAAGGTC	GCGTCGCAGG	TTGTGAGCAA	1140
TGCCTACCTC	GGCTCAGGGG	TGGCCCCGT	GCCAGAGATG	GTGGAGCGCG	GCATGGCCGT	1200

GGGCATTGGA ACAGATAACG GGAATAGTAA TGACTCCGCA AACATGATCG GAGACATGAA	1260
GTTTATGGCC CATATTCAACC GCGCGGTGCA TCGGGATGCG GACGTGCTGA CCCCAGAGAA	1320
GATTCTTGAA ATGGCGACGA TCGATGGGC GCGTTCGTTG GGAATGGACC ACGAGATTGG	1380
TTCCATCGAA ACCGGCAAGC GCGCGGACCT TATCCTGCTT GACCTGCGTC ACCTCAGACG	1440
ACTCTCACAT CATTGGCGG CCACGATCGT GTTTCAGGCT TACGGCAATG AGGTGGACAC	1500
TGTCCTGATT GACGGAAACG TTGTGATGGA GAAACGCCGC TTGAGCTTTC TTCCCCCTGA	1560
ACGTGAGTTG GCGTTCCCTTG AGGAAGCGCA GAGCCGCGCC ACAGCTATTT TGCAGCGGGC	1620
GAACATGGTG GCTAACCCAG CTTGGCGCAG CCTCTAGGAA ATGACGCCGT TGCTGCATCC	1680
GCCGCCCTT GAGGAAATCG CTGCCATCTT GGCGCGGCTC GGATTGGGG GCGGACATGA	1740
CCTTGATGGA TACAGAATTG CCATGAATGC GGCACCTCCG TCCTTCGCTC GTGTGGAATC	1800
GTTGGTAGGT GAGGGTCGAC TGCAGGGCGCC AGCTTCCCGA AGAGGTGAAA GGCCCGAG	1858

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gln Thr Leu Ser Ile Gln His Gly Thr Leu Val Thr Met Asp Gln
1 5 10 15

Tyr Arg Arg Val Leu Gly Asp Ser Trp Val His Val Gln Asp Gly Arg
20 25 30

Ile Val Ala Leu Gly Val His Ala Glu Ser Val Pro Pro Pro Ala Asp
35 40 45

Arg Val Ile Asp Ala Arg Gly Lys Val Val Leu Pro Gly Phe Ile Asn
50 55 60

Ala His Thr His Val Asn Gln Ile Leu Leu Arg Gly Gly Pro Ser His
65 70 75 80

Gly Arg Gln Phe Tyr Asp Trp Leu Phe Asn Val Val Tyr Pro Gly Gln
 85 90 95

Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu Tyr Cys
 100 105 110

Ala Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn Ala Asp
 115 120 125

Ser Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala Val Tyr Gly
 130 135 140

Glu Val Gly Val Arg Val Val Tyr Ala Arg Met Phe Phe Asp Arg Met
 145 150 155 160

Asp Gly Arg Ile Gln Gly Tyr Val Asp Ala Leu Lys Ala Arg Ser Pro
 165 170 175

Gln Val Glu Leu Cys Ser Ile Met Glu Glu Thr Ala Val Ala Lys Asp
 180 185 190

Arg Ile Thr Ala Leu Ser Asp Gln Tyr His Gly Thr Ala Gly Gly Arg
 195 200 205

Ile Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val Thr Val Glu
 210 215 220

Gly Met Arg Trp Ala Gln Ala Phe Ala Arg Asp Arg Ala Val Met Trp
 225 230 235 240

Thr Leu His Met Ala Glu Ser Asp His Asp Glu Arg Ile His Gly Met
 245 250 255

Ser Pro Ala Glu Tyr Met Glu Cys Tyr Gly Leu Leu Asp Glu Arg Leu
 260 265 270

Gln Val Ala His Cys Val Tyr Phe Asp Arg Lys Asp Val Arg Leu Leu
 275 280 285

His Arg His Asn Val Lys Val Ala Ser Gln Val Val Ser Asn Ala Tyr
 290 295 300

Leu Gly Ser Gly Val Ala Pro Val Pro Glu Met Val Glu Arg Gly Met
 305 310 315 320

Ala Val Gly Ile Gly Thr Asp Asn Gly Asn Ser Asn Asp Ser Ala Asn
 325 330 335

Met Ile Gly Asp Met Lys Phe Met Ala His Ile His Arg Ala Val His
 340 345 350

Arg Asp Ala Asp Val Leu Thr Pro Glu Lys Ile Leu Glu Met Ala Thr
355 360 365

Ile Asp Gly Ala Arg Ser Leu Gly Met Asp His Glu Ile Gly Ser Ile
370 375 380

Glu Thr Gly Lys Arg Ala Asp Leu Ile Leu Leu Asp Leu Arg His Leu
385 390 395 400

Arg Arg Leu Ser His His Leu Ala Ala Thr Ile Val Phe Gln Ala Tyr
405 410 415

Gly Asn Glu Val Asp Thr Val Leu Ile Asp Gly Asn Val Val Met Glu
420 425 430

Asn Arg Arg Leu Ser Phe Leu Pro Pro Glu Arg Glu Leu Ala Phe Leu
435 440 445

Glu Glu Ala Gln Ser Arg Ala Thr Ala Ile Leu Gln Arg Ala Asn Met
450 455 460

Val Ala Asn Pro Ala Trp Arg Ser Leu
465 470